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MGD; MGI:1197527; Top3a.

InterPro; IPR003601; DNAtopI_DNA_bind.
InterPro; IPR003602; DNAtopI_DNA_bind.
InterPro; IPR00380; Pro_topoisomerase.
InterPro; IPR00380; Pro_topoisomerase.
InterPro; IPR002936; Toprim.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF01131; Topoisom_bac; 1.
Pfam; PF01131; Toprim; 1.
Pfam; PF01396; Zf-C4_Topoisom; 1.
Pfam; PF001396; Zf-C4_Topoisom; 1.
Pfam; PF001396; Zf-CCHC; 1.
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STRAIN-BALB/C; TISSUE-Testis;
MEDLINE-98201702; PubMed-9540825;
Seki T., Seki M., Katada T., Enomoto T.;
Seki M., Katada T., Enomoto T.;
Seki T., Seki M., 
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CATALYTIC ACTIVITY: ATP-independent breakage of DNA, followed by passage and rejoining.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS.
SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III T
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                                                                                                                                                                                    M00343; ZnF_C2HC;
PS00396; TOPOISO
   ; Topoisomerase;
362 362
658 685
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TOPOISOMERASE_I_PROK; 1.

OMETASE; DNA-binding; Repeat; Zinc-finger
362 DNA CLEAVAGE (BY SIMILARITY).
685 C4-TYPE (POTENTIAL).
925 2 X 27 AA APPROXIMATE REPEATS
841 1.
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39, Last sequence update)
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III alpha (EC 5.99.1.2).
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                                                                                                                                                                      DEALAQYFGNGTELAQQEDIYPAMPEPIRKCPQCNKDMVLKTKKNGGFYLSCMGFPECRS
                                                                                                                                                                                                                                                                                                                                  LVEGYDSMGYEMSKPDLRAELEADLKLICDGKKDKFVVLRQQVQKYKQVFIEAVAKAKKL
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                                       REQQCGFFQWVDENTAPGTSGAPSWTGDRGRTLESEARSKRPRASSSDMGSTAKKPRKCS
                                                                       PPGSSVGCPSSVGSHMDGFGSLGSDSDGGTPCLCGQPAVTRTVQKDGPNKGRQFHTCAKP
                                                                                     PLGASLGCPPGPGIHLGGFGNPGDGSGSGTSCLCSQPSVTRTVQKDGPNKGRQFHTCAKP
                                                                                                                      GESNSVTCNCGQEAVLLIVRKEGPNRGRQFFKCNGGSCNFFLWADSPNPGAGGPPALAYR
                                                                                                                                                                                                                       AVWFPDSVLEASRDNSVCSVCQPPPVYRLKLKFKRGSLPPAMPLEFVGCIGGCDETLKEI
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 LCHQPGHTRPFCPQNR
                         REQQCGFFQWVDENVAPGSFAAPAWPGGRGKAQRPEAASKRPRAGSSDAGSTVKKPRKCS
                                                                                                                                                                                               LDLRFSGGPPRASQPSGRLQANQSLNRMDNSQH---PQPADSRQTGSSKALAQTLPPPTAA
                                                                                                                                                                                                                                               AVWLPDSVLEASRDSSVCPVCQPHPVYRLKLKFKRGSLPPTMPLEFVCCIGGCDDTLREI
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8.8e-289;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A.,
RA Mannatides P.G., Scherer S.E., LIP.M., Hoskins R.A., Galle R.F.,
RA Mannatides P.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfelifer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Baytsktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Baytsktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Baytsktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Deviles P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borlova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borlova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borlova D., Botchan M.R., Bouck J., Brokstein P., Brottier S.M.,
RA Borlova D., Botchan M.R., Bouck J., Brokstein P., Brottier S.M.,
RA GLORK K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., McLeod M.F., McDevann C.,
RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Messor D.R., Pacleb J.M.,
RA Merishas R., Tettor C., Stapleton M., Skupsh M.F., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupsh M.F., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupsh M.F., Smith T.,
RA Shone B.C., Siden Klamos I., Singson M., Welson D.R., Pacleb J.M.,
RA Wang Z.-Y., Wassarman D.A., Weinstock R., Wang A.H., Wang X.,
RA Wang Y.-Y., Brotter C., Turner R., Venter E., Wang A.H., Wang Y.,
RA Wang K.H., Zhong W., Sungh M., Sh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA topoisomerase III alpha (EC 5.99.1.2).
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MEDLINE-20196006; PubMed-10731132;
MCONTINE-20196006; PubMed-10731132;
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DNA, followed by passage and rejoining.

MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME-SEVERED DNA STRAND (BY SIMILARITY).

SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
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melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1250
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EMBL; AE003663; AAF53813.1; ALT_SEQ.
FlyBase; EBgn0040268; Top3-alpha.
InterPro; IPR003601; DNAtopI_ATP_bind.
InterPro; IPR003602; DNAtopI_DNA_bind.
InterPro; IPR000380; Pro_topoisomerase.
InterPro; IPR002936; Toprim.
InterPro; IPR001878; Znf_CCHC.
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Pfam; PF01751; Toprim; 1.
Pfam; PF01396; Zf C4_Topoisom; 1.
Pfam; PF01396; Zf C4_Topoisom; 1.
PR.NTS; PR00417; PRTPISWRASEI.
SWART; SM00437; TOP1AC; 1.
SWART; SM00436; TOP1BC; 1.
SWART; SM00433; TOPIBC; 1.
SWART; SM00433; ZnF_C2HC; 1.
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ACT_SITE
SEQUENCE
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or send an email to license@isb-sib.ch).
446
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                                                                          506 TAPPLLTEADLIALMEKHGIGTDATHAEHINTIKERGYIGVL-DKGFLVPGVIGMGLYEG
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                                                                                                  SPPKLLTEADLIALMEKHGIGTDATHAEHIETIKARMYYGLTPDKRFL-PGHLGMGLVEG
                                                                                                                                                                AQSILERGGPTPRNGNKSDQAHPPIHPTKYTNNLQGDEQRLYEFIVRHFLACCSQDAQGQ 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVLCVAEKNDAAKGIADLLSNGRMRRREGLSKFNKIYEFDYHLYGQNVTMVMTSVSGHLL 67
                                                                                                                                                                                                                                                                                                                                                         GAAITRFQTMRLQRLFPEKIADKLISYGSCQIPTLGFVAERYKEIEAFVSEPFWKIKVLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIGYEIIDVCRAIKPNISVYRATFSEITTVAVRRALQQLGQPDKRQSDAVDVRTELDLRT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QLAFQVSYKNWRTVDPRSLFDAPVEKGVGSDYEPIKRTLEREVRGCQGLIIWTDCDREGE 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AHDFQMOFRKWQSCNPLVLFEAEIEKYCPENFVDIKKTLERETRQCQALVIWTDCDREGE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KYLNVAEKNDAAKTIAGLLSNGAAQRREGYSVYNKVFDFEAPVRGQNAKMVMTSVSGHMM 86
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PS00396; TOPOISOMERASE_I_PROK; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.7%; Score 2230.5; DB 1; 41.6%; Pred. No. 2.1e-136; Live 125; Mismatches 307;
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	 -!- SIMILARITY: BELONGS TO PROKARYOTIC FAMILY. 	გგ
۵	 -!- CATALYTIC ACTIVITY: ATP-independent breakage of single-strande DNA, followed by passage and rejoining. 	ရှိရှိ
	<pre>topoisomerase III."; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databa</pre>	R 자
		RT
	SEQUENCE FROM N.A. STRAIN-BRISTOL N2;	R R
	[1]	RN
ž	Rhabditidae; Peloderinae; Caenorhabditis.	288
V	Caenorhabditis elegans. Chromadorea: Dhahditida: Dhahditoida	200
	DNA topoisomerase III (EC 5.99.1.2).	GN DE
	30-MAY-2000 (Rel. 39, Last 30-MAY-2000 (Rel. 39, Last	DŢ DŢ
	30-MAY-2000 (Rel. 39,	DT AC
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	1212 GRSQPTAITSDGPKTRRCGLCRKEGHTRNKCPR 1244	Дb
	936 RSKRPRASSSDMGSTAKKPRKCSLCHQPGHTRPFC	Qy
1211	1158 ASQLTVRKDGPNQGRPFYAC-PTREKSCGFFKWGDEDQNQGAS-STSWGSANRNPP	Дb
935	876 SVTRTVQKDGPNKGRQFHTCAKPREQQCGFFQWVDENTAPGTSGAPSWTGDRGRTLESEA	Qy
1157	1100 RVVTLPSIQQSNSQRGQSSMRSNSSSTVTITQTKTKQQERNTATPGDGEEVMCNCGQL	밁
875	845 GCPPGPGIHLGGFGNPGDGSGSGTSCLCSQP	Qy
1099	1040 QPARQNTVRKNGPNLGRLYYKCPKPDECNFFQWADEPPSSAKSKNSTGSAPQSTTSWGSN	БР
844	790 QEAVILITVRKEGENRGRQFFKC-NGGSCNFFLWADSPNPGAGGPPALAYRPIGASI	Qy
1039	980 KADERPMLWGTRERASLGTAAPTPPPKPAAKRPRWDSVERDSTPPSSVPESETVLCTGCQ	фd
789	759SROTGSSKALAQTLP	Qy
979	920 SSSQPKTISMVPLDDDIAAAFAADDDAEFEALVNGGTMPTESNGDQQLDKSLSEWIKEQD	Дb
758	750 NSQHPQPAD	Qy
919	860 KTKEPKAAPNKKTSSKSSGSIRSFFTSAAPTNSASNGLDEFFDSNDGFEDAMLAAAESVE	В
749	730PRASQPSGRLQANQSLNRMD	Qy
859	800 GGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGKGKKPGGESKKSATKKPPNEPKPK	рь
729	730	δõ
799	741 L-PCDNLFRTTFNINLDSVKKVGGIVGEVRGGGGGFGPGPGGGGGSGRGAGSGGWSSGPGG	DЬ
729	710 IGGCDDTLREILDLRFSGGPSGGP	Qy
740	685 PDCKNAVWLPTECKDASVLDECCPTCGDGYRM-LKF-RLSTPYYRGVFGTPSGWYKTC	DЬ
709	656 PECRSAVWLPDSVLEASRDSSVCPVCQPHPVYRLKLKFKRGSLPPTMPLEFVCC	δõ
684	625 SARINETPAANSAVQEGADGSAPSHGIIQSIFQCPKCNEAPLALKPKKNQQGWYIGCNNF	Дb
655	605 AQYFGNGTELAQQEDIYPAMPEPIRKCPQCNK-DMVLKTKKN-GGFYLSCMGF	Qy
624	565 YDAMELALAKPQLRAEFELDLKLICQGQKDPKVVLTEQIAKYKQAYQQITDKITAMDAKI	DЬ

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Pfam; PF01751; Toprim; 1.
Pfam; PF01751; Toprim; 1.
PRINTS; PR00417; PRTPISMRASEI.
SMART; SM00437; TOPIAC; 1.
SMART; SM00436; TOPIBC; 1.
SMART; SM00493; TOPRIM; 1.
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ACT_SITE
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the Euro
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European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
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                                                                                                                                 GLVEGYDSMGYEMSKPDLRAELEADLKLICDGKKDKFVVLRQQVQKYKQVFIEAVAKAKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKVTHDHKDGIVEFNWKRHRLFNHTACLVLYQLCVEDPMATVVEVRSKPKSKWRPQALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIGAAFTREQTLRLQRIFFEVLAE----QLISYGSCQFFTLGFVVERFKAIQAFVFEIFH
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                                                                                                                                                                                                       WGAFAQSILERGGPTPRNGNKSDQAHPPIHPTKYT--NNLQGDEQRLYEFIVRHFLACCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLIVEHTRESHKVEFLWDRNRLFDRDTVDILHDECKETKEAHVEKVAKKPKSKWRPQALD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLAHDFOMOFRKWOSCNPLVLFEAEIEKYCPENFVDIKKTLERETROCOALVIWTDCDRE
SAVWLPDSVLEASRDSSVCPVCQPHPVYRLKLKFKRGSLPPTMPLEFVCCIGGCDD----
                                                                                                          ALVDGYDDMGFAMSKPDLRANLEIGLKEICDGRRQKQEVLDEQIGKYRAIFVESERKIGV
                                                                                                                                                                                    IGDGKTQAPDFLTEADLISLMDKYGIGTDATHAEHIEKIKTREYIGVRPDGKLIPSFLGL
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                                    LSQSLQRYLDKNNQAGGG----PGGP--
                                                                       LDEALAQYFGNGTELAQQEDIYPAMPEPIRKCPQCNKDMVLKTKKNGGFYLSCMGFPECR
                                                                                                                                                                                                                                                                                                                                     WGDFANEVLQ-NGVNPRNGRKSDEAHPPIHPLKFTEKHQLQGDDWKVYELVVRHFLACVS
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43.5%; Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 1;
4.1e-103;
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Query Match
Best Local
                                                                                                                                                              Pfam; PF01131; Topoisom_bac; 1.
Pfam; PF01751; Toprim; 1.
PRINTS; PR00417; PRTPISMRASEI.
SMART; SM00437; TOP1Ac; 1.
SMART; SM00436; TOP1Bc; 1.
SMART; SM00493; TOPRIM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOP3_SCHPO
060126;
30-MAY-2000
30-MAY-2000
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
DNA topoisomerase III (EC 5.99.1.2).
TOP3 OR SPBC16G5.12C.
                                                                      Isomerase;
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its cont modified and this statement is not removed. Usage by entitles requires a license agreement (See http://www.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases :- CATALYTIC ACTIVITY: ATP-independent breakage of sing DNA, followed by passage and rejoining.
-!- SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOI:
                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003601; DNAtopI_ATP_bind InterPro; IPR003602; DNAtopI_DNA_bind InterPro; IPR00380; Pro_topoisomeras
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF126287; AAD22485.2; -. EMBL; AL023554; CAA19038.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20042440; PubMed=10572171;
Maftahi M., Han C.S., Langston L.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reinhardt R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lyne M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Freyer G
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                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                        InterPro; IPR002936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lethality associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---TLREILDLRFSGGPPRASOPSGRLQANQSLNRMDNSQHPQPADSRQTGSSKALAQTL
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Similarity
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                                                                                                                                                 PS00396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . A . ;
                                                                   Topoisomerase; DNA-binding.
330 330 DNA CLEAVAGE (BY S. 622 AA; 71169 MW; EF291B1717EB58C0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.A.
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S
                                                                                                                                          TOPOISOMERASE_I_PROK; 1.
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24.5%;
42.2%;
                                                                                                                                                                                                                                                                                                                                      Pro_topoisomerase
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Score 1279; DB 1; Pred. No. 2.6e-75;
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There are no restrictions
ng as its content is in
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                                                                                            SIMILARITY).
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                                                                      CRC64;
                      Length
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TOP3_YEAST
P13099;
                                                                                                                                            eukaryotic topoisomerase.";
Cell 58:409-419(1989).
[2]
SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=89324087;
                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1990
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990
                                                                                                                                                                                                                               DLINE-89324087; PubMed-2546682;
llis J.W., Chrebet G., Brodsky G.,
hyper-recombination mutation in S.
                                                                                                                                                                                                                                                                                                                                                                                   JAN-1990 (Rel. 13, Created)
JAN-1990 (Rel. 13, Last sequence update)
OCT-1996 (Rel. 34, Last annotation update)
topoisomerase III (EC 5.99.1.2).
3 OR EDR1 OR YLR234W OR L8083.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQGQETTVEIDIAQEREVAHGLMILARNYLDVYPYDHW-SDKILPVYEQGSHFQPSTVEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YAEGLLAGDYRPPRKGKHNDRAHPPIHPVQMVHRSALPSQDHWKVYELITRRFLACCSDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAQSILERGGPTPRNGNKSDQAHPPIHPTKYTNNL---QGDEQRLYEFIVRHFLACCSQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRIGAAFTRFQTLRLQRIFPEVLAEQLISYGSCQFPTLGFVVERFKAIQAFVPEIFHRIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGEHIGVEISNVARASNPSIQVIRADFNNLERSHIISAAKRPRDVSKNAADAVDARIELD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLLAHDFQMQFRKWQSCNPLVLFEAEIEKYCPENFVDIKKTLERETRQCQALVIWTDCDR
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Matches
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EMBL; U19077; AAB67406.1; -.
PIR; A33169; ISBYT3.
SGD; S0004224; TOP3.
Interpro; IPR003601; DNAtopI_ATP_bind.
Interpro; IPR003602; DNAtopI_DNA_bind.
Interpro; IPR003602; DNAtopI_DNA_bind.
Interpro; IPR003809; Pro_topoisomerase.
Interpro; IPR002936; Toprim.
Pfam; PF01151; Toprim; 1.
Pfam; PF01751; Toprim; 1.
PRINTS; PR00417; PRTPISMRASEI.
SMART; SM00437; TOP1AG; 1.
SMART; SM00436; TOP1BG; 1.
SMART; SM00433; TOPIAG; 1.
SMART; SM00433; TOPIM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isomerase; Topoisomerase; DNA-binding.

ACT_SITE 356 356 DNA CLEAVAGE (BY SIMILARITY).

SEQUENCE 656 AA; 74370 MW; 51DF78936A88B4F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the
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European
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA, followed by passage and rejoining. SIMILARITY: BELONGS TO PROKARYOTIC TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIBOSOMAL DNA RINGS.
CATALYTIC ACTIVITY: ATP-independent breakage of
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                          MATVVEVRSKPKSKWRPQALDTVELEKLASRKLRINAKETMRIAEKLYTQGYISYPRTET
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                                                                                                                                                                                                                                                                                     KVLCVAEKNDAAKGIADLLSNGRMRRREGLSKFNKIYEFDYHLY-----GQNVTMVMTSV
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                                                                                          VVERFKAIQAFVPEIFHRIKVTHDHKD--GIVEFNWKRHRLFNHTACLVLYQLCVEDP--
                                                                                                                            RIEIDLRAGVTFTRLLTETLRNKLRNQATMTKDGAKHRGGNKNDSQVVSYGTCQFPTLGF
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                                                          VVDRFERIRNFVPEEFWYIQLVVENKDNGGTTTFQWDRGHLFDRLSVLTFYETCIETAGN
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Pred. No. 1.6e-68;
4; Mismatches 213
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binds in vitro
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EMBL

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Gaps

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HSSP; P06612; ÎECL.

MGD; MGI:1333803; Top3b.

InterPro; IPR003601; DNAtopI_ATP_bind.

InterPro; IPR003602; DNAtopI_NA_bind.

InterPro; IPR003602; DNAtopI_SOMERASE.

InterPro; IPR002306; Pro_topoisomerase.

InterPro; IPR002306; Toprim.

Pfam; PF01131; Topoisom_bac; 1.

Pfam; PF01131; Topoisom_bac; 1.

PRINTS; PR00417; PRTPISMRASEI.

SMART; SM00437; TOP1BC; 1.
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MEDILINE=99003190; PubMed=9786843;

Seki T., Seki M., Onodera R., Katada T., Enomoto T.;

Seki T., Seki M., Onodera R., Katada T., Enomoto T.;

Seki T., Seki M., Onodera R., Katada T., Enomoto T.;

Seki T., Seki M., Onodera R., Katada T., Enomoto T.;

Seki T., Seki M., Onodera R., Katada T., Enomoto T.;

Tolining of cDNA encoding a novel mouse DNA relaxing activity, whose message is highly expressed in the testis.";

J. Biol. Chem. 273:28553-28556(1998).

-I- FUNCTION: POSSESS NEGATIVELY SUPERCOILED DNA RELAXING ACTIVITY.

-I- CATALYTIC ACTIVITY: ATP-Independent breakage of single-stranded
                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MA topoisomerase III beta-1 (EC 5.99.1.2).
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TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS.
SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III 1
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TP3B_HUMAN
ID TP3B_HUMAN
ID TP3B_HOMAN
AC 095985; 0988
DT 30-MAY-2000
DT 30-MAY-2000
DT 01-MAR-2002
DE DNA topoisor
GN T0P3B1 OR T0

095985; Q9BUP5; 30-MAY-2000 (Re 30-MAY-2000 (Re 01-MAR-2002 (Re

(Rel.) (Rel.) (Rel.)

39, 39, 41, III

Created)

Last sequence update)
Last annotation update)
beta-1 (EC 5.99.1.2).

STANDARD;

PRT;

862

A

DNA topoisomerase TOP3B1 OR TOP3B.

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PROSITE; PS00396; TOPOISOMERASE_I_PROK; 1.

Isomerase; Topoisomerase; DNA-binding.

ACT_SITE 336 DNA CLEAVAGE
SEQUENCE 862 AA; 96949 MW; D2C05429F79
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nes 276; Conserv
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                                                                                                                                                          LPGHLGMGLVEGYDSMGYEMSKPDLRAELEADLKLICDGKKDKFVVLRQQVQKYKQVFIE
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                                                   ----HCDETYTLPQNGTIKLYKELRCPLDDFELVLWSSGSRGKSYPLCPYCYNHPPFR-D
                                                                                                        FVDSIAGMDELMEVSF---SPLA-----
                                                                                                                                                                                                                                                                    TVSHDCKYLQSTISFRIGPEHFTCMGKTVISPGFTEIMP----WQSVPLEESLPTCQKGDT
                                                                                                                                                                                                                                                                                            CCSQDAQGQETTVEIDIAQERFVAHGLMILARNYLDVYPYDHWS----DKILPVYEQGSH
                                                                                                                                                                                                                                                                                                                        HPYWADSVKQLLAEGINRPRKGHDAGD-HPPITPMKSATEAELGGDAWRLYEYITRHFIA
                                                                                                                                                                                                                                                                                                                                               DPRWGAFAQSILERGGPTPRNGNKSDQAHPPIHPTKYTN--NLQGDEQRLYEFIVRHFLA
                                                                                                                                                                                                                                                                                                                                                                           ALNTVEMLRVASSALGMGPQHAMQIAERLYTQGYISYPRTETTHYPENFDLKGSLRQQAN
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MKKGMGCNECTHP----TCQHSLSMLGIGQCVECENGVLVLDPTSGP
                                                                                                                                AVAKAKKLDEALAQYFGNGTELAQQEDIYPAMPEPIRKCPQCNKDMVLKTKKNGGFYLSC
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36.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D2C05429F79FD5CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 311;
                                                                                                        -ATGKPLSRCGKCHRFMKYIQAKPSRLHCS-
                                                                              -VL--EASRDSS--VCPVCQPHPVYRLK
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InterPro; IPR003601; DNAtopI_ATP_InterPro; IPR003602; DNAtopI_DNA_InterPro; IPR000380; Pro_topoison_InterPro; IPR000380; Pro_topoison_InterPro; IPR002936; Toprim.
Pfam; PF01131; Topoisom_bac; 1.
Pfam; PF01751; Toprim; 1.
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PRINTS;
SMART; S
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VARSPLIC
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or send a
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Riou J.F., Goulaouic
Submitted (FEB-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97228902; PubMed-9074928;
Kawasaki K., Minoshima S., Nakato
Schmeits J.L., Wang J., Shimizu N
SEQUENCE
                                                                                                 PROSITE;
                                                                                                                    SMART;
                                                                                                                                                                                                                                                                                                                                                     between
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Submitted (FEB-2001)
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                                                                 VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "One-megabase sequence analysis gene locus.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=99128286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   SPECIFICITY: THE TOP3B ISOFORMS HAVE DIFFERENT TISSUE SPECIFICITIES. ISOFORM 1 IS FOUND IN TESTIS, HEART AND SKELET MUSCLE. A 4 KB TRANSCRIPT, WHICH PROBABLY REPRESENTS ISOFORM FOUND IN THYMUS, KIDNEY AND PANCREAS.
SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOTSOMEDSOME FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   new human
                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no restructy py non-profit institutions as long as its content
                                                                                                                                                                                                                      603582;
                                                                                                                                                                                                                                         AF053082;
AF017146;
AF125216;
BC002432;
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                                                                                                                    SM00437;
SM00436;
                                                                                                                                                                                                                              P06612; 1ECL.
                                                                                                                                                                                                                                                                                                 an
                                                                                                                                           PR00417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acids
                                                                                                 PS00396;
                                                                                                                                                                                                                                                                                                         and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu Y.,
                                                                                                                                                                                                                                                                                                email to license@isb-sib.ch).
                                                                                     Topoisomerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7:250-261(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      u Y., Hasselblatt K.T., M
topoisomerase III that i
s Res. 27:993-1000(1999).
                                                                                                                                                                                                                                          AAD15791.1; -. AAD01614.1; -. AAD29670.1; -. AAH02432.1; -.
                                                                                                         TOPRIM;
                                                                                                                              TOP1Ac;
                                                                                                                     TOP1Bc;
                                                                                                                                           PRTPISMRASEI.
                                                                                              TOPOISOMERASE_I_PROK;
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365
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730
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96661
                                                                                                                                                                          Pro_topoisomerase.
Toprim.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Grondard the EMBL/G
                 e; DNA-binding; Alternative splicing.
DNA CLEAVAGE (BY SIMILARITY).
GMCCNECTHPSCOHSLSMLGIGCVECE -> GI
TGSCSLFSVPTPALHQAGL (IN ISOFORM 2
MISSING (IN ISOFORM 2).
GMGCN -> VVPCV (IN ISOFORM 3).
MISSING (IN ISOFORM 3).
Z
                                                                                                                                                                                                                                                                                                                     is not removed.
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          (IN ISOFORM 3).
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Best Local
                                      Drosophila melanogaster (Fruit fly)
Eukaryota; Metazoa; Arthropoda; Trac
Pterygota; Neoptera; Endopterygota;
                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
DNA topoisomerase III beta (EC 5.99.1.2).
TOP3-BETA OR TOP3 OR CG3458.
                                                                                                            O96651; Q9W416;
30-MAY-2000 (Rel. 39,
16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                      DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QRPLALNTVEMLRVASSSLGMGPQHAMQTAERLYTQGYISYPRTETTHYPENFDLKGSLR 355
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                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -KDRSLLLDWDRVRVFDREIAQMFLNMTKLEKEAQVEATSRKEKAK
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Pred. No. 2
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                                                       Tracheata;
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                                                                                                                                                                        875
                                                                                               update)
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.3e-61;
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                                                       Hexapoda;
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Ephydroidea; Dro NCBI_TaxID=7227 [1]

Drosophilidae;

Diptera;

Brachycera;

Muscomorpha;

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RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
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RA McIkulov G., Milshina N.Y., Mobarry C., Morris J., McPherson D.L.,
RA Munnt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Neltman G.S., Pan S., Pollard J., Puri V., Resse M.G.,
RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
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A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
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A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
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Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Burthi S.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Bodson K.J. Bouck J., Downes M., Dugan-Rocha S., bunkov B.C., Dunn P.,
Bashan R.J., Bouck J., Dugan-Rocha S., bunkov B.C., Dunn P.,
Bashan R.J., Bouck J., Dugan-Rocha S., bunkov B.C., Dunn P.,
Bashan R.J., Bashan R.J., Bouck J., Dugan-Rocha S., bunkov B.C., Dunn P.,
Bashan R.J., Bashan R.J., Bouck J., Dugan-Rocha S., bunkov B.C., Dunn P.,
Bashan R.J., Bashan R.J.
                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wilson T.M., Chen A.D., Hsieh T.-S.;
"Cloning and characterization of Drosophila topoisomerase
"Claring and orbaracterization of bypernegatively supercoiled DNA.";
J. Biol. Chem. 275:1533-1540(2000).
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                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: WEAKLY RELAXES NEGATIVE SUPERCOILS AND DISPLAYS A
DISTINCT PREFERENCE FOR BINDING SINGLE-STRANDED DNA.
CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded
DNA, followed by passage and rejoining.
DEVELOPMENTAL STAGE: EXPRESSED DURING THE FIRST 6 HOURS OF
DEVELOPMENTAL STAGE: EXPRESSED DURING THE FIRST 6 HOURS OF
DEMBRYONIC DEVELOPMENT, LEVELS DECLINE DURING LARVAL AND PUPAL
STAGES TO INCREASE AGAIN DURING ADULTHOOD.
MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA
BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN DNA LINK, IN
                                                                                                                                                                                                                                                                                                              WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME-SEVERED DNA STRAND (BY SIMILARITY). SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
AF099909;
AE003437;
                                                                          s requires a license agreement (s an email to license@isb-sib.ch).
AAD13219.
AAF46144.
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                                                                                                  (See http://www.isb-sib.ch/announce/
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InterPro; IPR000380;
InterPro; IPR002936;
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875 AA;
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Pfam; PF01131; Topoisom_bac; 1.
Pfam; PF01751; Toprim; 1.
Pfam; PF01751; Toprim; 1.
PRINTS; PR00417; PRTPISMRASEI.
SMART; SM00436; TOP1BC; 1.
SMART; SM00436; TOP1BC; 1.
SMART; SM00493; TOPRIM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 HVMSLDFNKKYNCWDKVDPIQLFGCATEKKETNPKQNMRKFLAHEARGCDYLVLWLDCDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKSVLMVAEKPSLAASLAGILSNGRCTAKRGTGNGCSTHEWTGNFRNEGSVHFRMTSVCG
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                                                                                                                                                   VAKAKKLDEALAQYFGNGTELAQQEDIYPAMPEPIRKCPQCNKDMYLKTKKNGGFYLSCM
                                                                                                                                                                                                                                                                                        DFGEEARSIL - -GDIQTPRKG - KDAGDHPPITPMKLGNRSDFDRDTWRVYEFICRHFMGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RWGAFAQSILERGG-PTPRNGNKSDQAHPPIHPTKYTN--NLQGDEQRLYEFIVRHFLAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WHLQLLAGQPE--VTLEWARGRVFKKDIAIMLLNRVKEHKKATVESVASKEAYKSKPQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QELDLRIGAAFTREQTLRLQRIFPEVLAEQLISYGSCQFPTLGFVVERFKAIQAFVPEIF
                                                                                                                                                                                                                              PGHLGMGLVEGYDSMGYEMSKPDLRAELEADLKLICDGKKDKFVVLRQQVQKYKQVFIEA
                                                                                                                                                                                                                                                                      AINDVRLIESQTGPPDYLTESELITLMEEHGIGTDASIPVHINNICQRNYVHIENGRKLM
                                                                                                                                                                                                                                                                                                                                                   VSRDLKYRVTTAKLSVGMETFSCTASVLIDAGFTKVMT---WSAFGKDEPQPPFVQGTQV
                                                                                                                                                                                                                                                                                                                                                                                     CSQDAQGQETTVEIDIAQERFVAHGLMILARNYLDVYPYDHWS----DKILPVYEQGSHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HRIKVTHDHKDGIVEFNWKRHRLFNHTACLVLYQLCVEDPMATVVEVRSKPKSKWRPQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QELDLRIGCAFTRFQTKFFQDRYGD-LDSSLISYGPCQTPTLGFCVKRHDDIQTFKPESF
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FKRGSLPPTMPLEFVCCIGGCDDTLREILDLRFSGGPPRASQPSGRLQANQSLNRMDNSQ
                                      --- HCDETYALPIGNVKVYREFKCPLDDFDLLAFSTGVKGRSYPFCPYCYNHP
                                                                                                                                                                                         PTTLGTVLVHGYQKIDPELVLPTMRTEVERMLTLIAQGSANFQDVLRHAIKIFKLKFMYF
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                                                                                                               KNIDSMDALFEVSFSPLAESGKAH------SRCGKCRRYMKYIQTKPARLHCS--
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859 G
747 V
96973 MW;
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DNAtopI_ATP_bind
DNAtopI_DNA_bind
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Pred. No. 1
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1.7e-58;
hes 376;
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RESULT 10
TOP1_ARCFU
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16-OCT-2001 (Rel. 40)
DNA topoisomerase I (
Untwisting enz"
TOPA OR AFT'
AFT'
                                                                                                                                                             entities
or send a
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Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson J.D., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Ouackenbush J., Lee N.H., Sutton G.G., Gill S. Fleischmann R.D., Ouackenbush J., Lee N.H., Sutton G.G., Gill S. Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B. Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zh Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R., Venter J.
                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
-!- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES CONVERSION OF ONE TOPOISOMERASES.
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                                       InterPro;
                                                              InterPro;
                                                                                     TIGR;
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Archaea; Euryarchaeota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                          SIMILARITY).

CATALYTIC ACTIVITY: ATP-independent breakage of single-strang DNA, followed by passage and rejoining.

MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, II WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOS! AT ONE END OF THE ENZYME SEVERED DNA STRAND.

SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
                                                                                                                                                                                                                                                                                                                              FAMILY.
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                                                                                 AF1806;
                                                                                                                       AE000978;
                                                                                                    P06612; 1ECL.
                                                                                                                                                             s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM N.A
    IPR003601;
IPR003602;
IPR000380;
IPR000386;
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                                                                                                                         AAB89443.1;
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40, Last sequence update)
40, Last annotation update)
1 (EC 5.99.1.2) (Omega-protein)
                  DNAtopI_ATP_bind.
DNAtopI_DNA_bind.
Pro_topoisomerase
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Pfam; PF01751; Toprim; 1.
Pfam; PF01396; zf-c4_Topoisom; 1
PRINTS; PR00417; PRTPISMRASEI.
SMART; SM00437; TOPLAC; 1.
SMART; SM00436; TOPLBC; 1.
SMART; SM00439; TOPRIM; 1.
TOP1_THEAC
Q9HM08;
16-OCT-2001
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Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                          FTLPLPQNGTLYITAKQ---
                                                                                                                                                                                  SAVWLPDS - - - VLEASRDSSVCPVCQPHPVYRLKLKFKRG
                                                                                                                                                                                                                                                                                                       SVINVLKETAETITLPDMTAKLENEMDLIAEGKKREPEVVDESREMULQI-LRAI-DYRK
                                                                                                                                                                                                                                                                                                                                                                                                         MVDGETSPPKLLTEADLIALMEKHGIGTDATHAEHIETIKARMYVGLTPDKRFLPGHLGM : : | | : | | : | | : | | | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---EAQIVLSQDKITPSRGRRETKDHPPIYPTGVAKRGELSKDEWTIYELVVRRFLATLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WGAFAQSILERGGPTPRNGNKSDQAHPPIHPTKYT--NNLQGDEQRLYEFIVRHFLACCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEFLREASKFM--SPHKAMNIAETLYMNGYISYPRTDNTVYPPTINLIEIVSALSSVFPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVEALEIVKSVNPTVKVDRVRYSAVTEKEIRSAFSKPVKVDFNLANAALARQKIDLIWGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GFEIIHVCKAVKPNLQVLRARFSEITPHAVRTACENLTEPDQRVSDAVDVRQELDLRIGA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DFQMQFRKWQSCNPLVLFEAEIEKYCPENFVDIKKTLERETRQCQALVIWTDCDREGENI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LCVAEKNDAAKGIADLLSNGRMRRREGLSKFNKIYEFDYHLYGQNVTMVMTSVSGHLLAH 69
                                                                                                                                                                                                                         LSKDL---
                                                                                                                                                                                                                                                               LDEALAQYFGNGTELAQQEDIYPAMPEPIRKCPQCNKDMVLKTKKNGGFYLSCMGFPECR
                                                                                                                                                                                                                                                                                                                                               GLVEGYDSMGYEMSKPDLRAELEADLKLICDGKKDKFVVLRQQVQKYKQVFIEAVAKAKK
                                                                                                                                                                                                                                                                                                                                                                                      LEEKETKPPGRYSASSLIKMMEKLNLGTKSTRHEIIQKLVSRRYIHGNP---FRPSETAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PKAVWDVRRVVLDSNGVKFVANGRQLVEAGWRDIYIYSKAEETELPLLKKGDVLRILKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QDAQGQETTVEIDIAQERFVAHGLMILARNYLDVYPYDHWSDKILPVYEQGSHFQPSTVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VELEKLASRKLRINAKETMRIAEKLYTQGYISYPRTETNIFPRDLNLTVLVEQ-OTPDPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDGIVEFNWKRH------RLFNHTACLVLYQLCVEDPMATVVEVRSKPKSKWRPQALDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLTRLISVHSGR-----MGKDFLSVGRVQTPTLRLIVDRELEIQNFKPEKYYEIFAEF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AFTRFQTLRLQRIFPEVLAEQLISYGSCQFPTLGFVVERFKAIQAFVPEIFHRIKVTHDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DFPKELNNWTKTPLEKLLQAELVKKVKER--TISSILKEIAKKADRVTVATDYDREGELI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIITEKDNTARRIASILFKDVKTLKKGRVSY-----YHSPSNDAYVV--GLKGHIVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -EGFIAKHPKRYGSKEEAEKLFAKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          se; Topoisomerase; DNA-binding; Zinc-finger; Metal-binding; Complete proteome.
583 610 C4-TYPE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    663 AA;
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                         STANDARD;
                                                                                                                                                                                                                         REGVKKDKI --
  40, Created)
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653 C
306 D
76017 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136; Mismatches
                                                                                                                                          -CKEHEIKEVKIRTKKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C4-TYPE 1.
C4-TYPE 2 (ATYPICAL).
DNA CLEAVAGE (BY SIMILARITY).
OA07E4FD20871BAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>.</u>
                                         PRT;
                                                                                                                                                                                                                         -VGKCPECGGELVVRQSKAGKRFIGCSNYPDCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     688; DB 1;
No. 4.5e-37;
                                         770
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--ETAKVEEFTRRRMEENRPTPFNT

302

227 249 174

419

333 361 275

390

450

298;

74;

Gaps

18;

56

Length Indels

AA

644

659 565 599

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В
                                                             Qy
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                                                                                                                         Q
                                                                                                                                                            Query Match
Best Local S
Matches 205
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Pfam; PF01751; Toprim; 1.
Pfam; PF01751; Toprim; 1.
Pfam; PF01196; zf-C4_Topoisom; 1.
PfanyTs; PR00417; PRTPISMRASEI.
SMART; SM00437; TOP1BC; 1.
SMART; SM00436; TOP1BC; 1.
                                                                                                                                                                                                                                                                       Repeat;
ZN_FING
ZN_FING
                                                                                                                                                                                                                                       ZN_FING
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AL445063; CAC11211.1;
InterPro; IPR003601; DNAtopt_ATP_bind.
InterPro; IPR003602; DNAtopt_DNA_bind.
InterPro; IPR000380; Pro_topoisomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mewes H.-W., Frishman The genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 407:508-513(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acidophilum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruepp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermoplasma acidophilum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPA OR TA0063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA topoisomerase
                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Untwisting
   125
                                   60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA, followed by passage and rejoining.

MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT SIMULANEOUSLY FORMS A PROTEIN-DNA LINK, IN WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME-SEVERED DNA STRAND.

SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: ATP-independent breakage of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: THE REACTION CATALYZED BY T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY)
                                                                                                IIIAEKADAGRRIAYFLSGGQVKSHR--AKGTSYLEFEYN--GSKTYLI--PLSGHIVEA
EGENIGFEITHVCKAVKPNLQVLRARFSEITPHAVRTACENLTEPDQRVSDAVDVRQELD
                                                                                                                             LCVAEKNDAAKGIADLLSNGRMRRREGLSKFNKIYEFDYHLYGQNVTMVMTSVSGHLLAH
                                 DFESGYSDWNKIDLSDLIDARIVK-----NIKNKVAYQTLQAFRGKVEEIVIATDYDR
                                                             DFQMQFRKWQSCNPLVLFEAEIEKYCPENFVDIKKTLERETRQC-----QALVIWTDCDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volk H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister genome sequence of the thermoacidophilic scavenger Therm
                                                                                                                                                                                                                                                                                                                                                       SM00493; TOPRIM;
                                                                                                                                                                                                                                                                                                       Complete proteome.
                                                                                                                                                            Similarity 26.5
05; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR002936; Toprim.
                                                                                                                                                                                                                                                                                                                         Topoisomerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 41, Last annotation update)
merase I (EC 5.99.1.2) (Omega-protein)
enzyme) (Swivelase).
                                                                                                                                                                                                                                                                                                                                      TOPOISOMERASE_I_PROK;
                                                                                                                                                                                                                                                                       700
                                                                                                                                                                                                                            87667
                                                                                                                                                         12.5%; Score 653; DE 26.5%; Pred. No. 1e-3 tive 130; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermoplasmales;
                                                                                                                                                                                                                            M.
                                                                                                                                                                                                                                                                                                                       DNA-binding; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                   C4-TYPE 1.
C4-TYPE 2.
C4-TYPE 3.
DNA CLEAVAGE (BY SIMILARITY).
75DA8DD7BC3B8A22 CRC64;
                                                                                                                                                                           1e-34;
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R OF DNA TO ANOTHER
                                                                                                                                                                                                                                                                                                                                      FALSE_NEG
                                                                                                                                                                                            В
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                                                                                                                                                              329;
                                                                                                                                                                                         1;
                                                                                                                                                                                       Length 770;
                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single-stranded
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                                                                                                                                                            110;
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                                                                                                                                                                                                                                                                                                            484
                                                                                                                                                                                                                                                                                                                                                                                                                                                   365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185
                                                                                                    CPQC--
                                                                                                                                                                       LAQYFGNGTEL-----
                                                                                                                                                                                                                                                                                                                                                                                                                YVKEIETFDRILPSRGRIETTDHPPIYPVDSPKEQLKGDYGRVYDLILRHFLSTLYRDGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGELIGVEALDIIKEGKE--EIRRAKFSALTKNEILDSFKNLIGVNYSLADAADARESID
SNYPKCTVTYPLP-QMGRITKTGEVCPYCGA-PILALSRNGRKWKFCPNMQCEY 746
                                  MGFPECRSAVWLPDSVLEASRDSSVCPVCQPHPVYRLKLKFKRGSLPPTMPLEF 706
                                                                                                                                                                                                       AVRSVNSHIADPEMTAKLEEDMDRIEKNEMSKNDVVEESKKMLHEVLSHFLTKTADVKDI
                                                                                                                                                                                                                                      GYDSMGYEMSKPDLRAELEADLKLICDGKKDKFVVLRQQVQKYKQVFIEAVAKAKKLDEA
                                                                                                                                                                                                                                                                                             ETSPPKLLTEADLIALMEKHGIGTDATHAEHIETIKARMYVGLTPDKRFLPGHLGMGLVE
                                                                                                                                                                                                                                                                                                                                            KTVAEAEIYVNGYTFKAAGQHTTDRGWTEIYGYDP-KDVYLPELTEGEDLKAIDWNIQRE
                                                                                                                                                                                                                                                                                                                                                                                                                                               FAQSILERGGPTPRNGNKSDQAHPPIHPT-KYTNNLQGDEQRLYEFIVRHFLACCSQDAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLREASR-IGIMPTKAMSIAENLYMRGLISYPRTDNTVYPRSINLKSVL-KKLENTAYSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEKLASRKLRINAKETMRIAEKLYTQGYISYPRTETNIFPRDLNLTVLVEQQTPDPRWGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTFD-KDGQFKARYPENIKDQDTA-EKIYE-AIKGKNGRVSSYTSKEDHIRRPAPFSTTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTHDHKDGIVEFNWKRHRLFNHTACLVLYQLCVEDPMATVVEVRSKPKSKWRPQALDTVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIWGSVLTRFFSVTTGR-----LGKSFLSAGRVQTPTLAIVVDREREIQSFRPERYWTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRIGAAFTRFQTLRLQRIFPEVLAEQLISYGSCQFPTLGFVVERFKAIQAFVPEIFHRIK
                                                                    CPVCGLPMIKIIRKGQSPEIKCIDPDCSYNRENEDYGECPADHGRLVLRQSKYGKRFLGC
                                                                                                                                     ITKGINAGQEIGDCPFHEGKKIMVIRDRFTYTVRCED--PSCKINFRIKRNGSITLSDQK
                                                                                                                                                                                                                                                                          ETKPPPRYDMSSLLKKMEELNLGTKSTRHDIIGKLIERGFIEGNPVK--
                                                                                                                                                                                                                                                                                                                                                                              GQETTVEIDIAQERFVAHGLMILARNYLDVYPYDHWSDKILPVYEQGSHFQPSTVEMVDG
                                                                                                                                                                     ----AQQEDIYPAMPEPIR----K
                                                                                                  -PTPLGMAFID
                                                                                                                                                                                                    576
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                                                                                                                                                                     630
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RESULT 12
TOP1_PYRAB
                                                                                                                                                                                                                                                                                 (Untwisting enzyme) (Swivelase) TOPA OR PAB1430.
                                                                                                                                                                                                                                                                                                                                        16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                  "Pyrococcus abyssi genome sequence: insights into archaeal structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEAR CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER
                                                                                                                                                                                                                                                Pyrococcus abyssi.
Archaea; Euryarchaeota;
NCBI_TaxID=29292;
                                                                                                                                                                                                                                                                                                                                                                                 Q9UYS8;
                                                                                                                                                                                                                                                                                                                                                                                                  TOP1_PYRAB
                                                                                                                                                                                                        STRAIN-ORSAY;
                                                                                                                                                                                            Heilig
                                                                                                                                                                                                                      SEQUENCE FROM
SIMILARITY).

CATALITIC ACTIVITY: ATP-independent breakage of single-strange of locality of the passage and rejoining.

DNA, followed by passage and rejoining.

MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A LINK, II WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSIAT ONE END OF THE ENZYME IS SEVERED DNA STRAND.

SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
                                                                                                                                                                                            R.;
                                                                                                                                                                                                                                                                                                                                        (Rel.
                                                                                                                                                                                                                      N.A.
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ISOMErase; Topoisomerase; DNA-binding; Zinc-finger; Metal-binding;
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"Complete sequence and gene organization of the genome of a h
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MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME-SEVERED DNA STRAND.

SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
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m; PF01751; Toprim; 1.
m; PF01396; zf-C4_Topoisom; 1.
NTS; PR00417; PRTPISMRASEI.
RT; SM00437; TOP1AC; 1. P06612; AP000003; SM00437; SM00436; an email to license@isb-sib.ch). requires a 1ECL. BAA29711.1; license agreement (See http://www.isb-sib.ch/announce/ Pro_topoisomerase DNAtopI_ATP_bind DNAtopI_DNA_bind

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLCVAEKNDAAKGIADLLSNGRMRRREGLSKFNKIYEFDYHLYGQNVTMVMTSVSGHLL-
                                                                                                            T---NKTCCNGAPVVIIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YDTEGEVIGYTALKYACGVDPRV-AKRMKFSALTKRDLLNAWRNL-EPTINFGMANAGIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAPKRDVFGYPIFDIEW-----VPVYIAEKGKEYAREYIKALSVLAKRVRE----FIVACD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILITAEKPNVARKTAGALSERRPIKK---SLFGVPY---YEIFREGKKLIVASAVGHLYG
                                                                                                                                     TMPLEFVCCIGGCDDTLRE
                                                                                                                                                                                                                           YKQVFIEAVAKAKKLDEALAQYFGNGTELAQ----QEDIYPAMPEPIRKCPQCNKDMVLK
                                                                                                                                                                                                                                                            GKKSIKVTP-
                                                                                                                                                                                                                                                                                 LTPDKRFLPGHLGMGLVEGYDSMGYEMSKPDLRAELEADLKLICDGKKDKFVVLRQQVQK
                                                                                                                                                                                                                                                                                                        EFFIGERIKVIQVKREKKKTKPPARYSPAAVIKKMEDLGLGTKATRAQILETLYQRGYIE
                                                                                                                                                                                                                                                                                                                                 VYEQGSHFQPSTVEMVDGETSPPKLLTEADLIALMEKHGIGTDATHAEHIETIKARMYVG
                                                                                                                                                                                                                                                                                                                                                                     YEFIVRHFLACCSQDAQGQETTVEIDIAQERFVAHGLMILARNYLDVY-PYDHWSDKILP
                                                                                                                                                                                                                                                                                                                                                                                                                                TVLVEQQTPDPRWGAFAQSILERGGPTPRNGNKSDQAHPPIHPT---KYTNNLQGDEQRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPKSKWRPQALDTVELEKLASRKLRINAKETMRIAEKLYTQGYISYPRTETNIFPRDLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YWVIKLIFEKNGQKFTANYEKDKIWEE------EEGKRIVLEVKKSIPRVSNVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FHRIKVTHDHKDGIVEFNWKRHRLFNHTACLVLYQLCVEDPMATVVEVRS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RHILDWYWGVNLSRALTHAIKKASGKWV----VLSTGRVQGPTLKFLVEREREIQSFVPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RQELDLRIGAAFTRFQTLRLQRIFPEVLAEQLISYGSCQFPTLGFVVERFKAIQAFVPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----AHDFQMQFRKWQSCNPLVLFEAEIEKYCPENFVDIKKTLERETRQCQALVIWTD
                                                                                                                                                             YNKKTGKRFVGCSNWPKC----
                                                                                                                                                                                                                                                                                                                                                         YDMIVRRFLAVFMEPAIRESVKVTIRAGPHKFFLSGGRTVKKGWLSVYGKYVKFEEVTLP
                                                                                                                                                                                                                                                                                                                                                                                                         RMIIQNLAKMPQYRPYAHILLGLPELKPVEGKKEDPAHPAIYPTGEIPRPGDLTKDEEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRQKRTPPHPFDLGTLQREAYSAFGFSPKKTLDIAQSLYEKGFSSYPRTESQKLPRNINF
                                                                                                                                                                                  -TKKNGGFYLSCMGFPECRSAVWLPDSVLEASRDSSVCPVCQPHPVYRLKLKFKRGSLPP
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PS00396; TOPOISOMERASE_I_PROK; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Topoisomerase;
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653
317
  (Rel.
(Rel.
(Rel.
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                                                  STANDARD;
                                                                                                                                                                                                                                                          -LGMKVIETLEKYVPEIISVELTREFEKKMELIMEGRLTKEEVIEEAKER
  40,
40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                634
678
317
                                                                                                                                                                                                           -LEEFKKRELEIGIELAKIVVGEDEVKPLV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.3%;
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Created)
Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C4-TYPE 1.
C4-TYPE 2 (ATYPICAL).
DNA_CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
                                                  PRT;
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               update)
                                                  761
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                                                                                                                                                           -DVTYPILQ-----
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                                                                                                                                                                                                           -VGKCPKCGGDLIVK
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                                                                                                                                                             -RGEIIP
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Qy

VRKVLCVAEKNDAAKGIADLLSNGRMRRREGLSKFNKIYEFDYHLYGQNVTMVMTSVSGH

В

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IMTALIICEKPSVAKKIANALGKAKKKSIDGVPY-----

-YELERDGKKIIVASAVGH

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BARROSOS AN ARANA ARANA ARANA SOS SOS SOS SOS ARANA AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "T "Complete genome sequence of the methanogenic archaeon, Methanococcut Jannaschii.";

I Science 273:1058-1073(1996).

L Science 273:1058-1073(1996).

C -!- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER (BY SIMILARITY).

C -!- GATALYTIC ACTIVITY: ATP-independent breakage of single-stranded DNA, FOllowed by passage and rejoining.

C -!- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBOWE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN DNA LINK, IN WHICH A TYROSYL OXYGEN UN THE ENZYME IS JOINED TO A DNA PHOSPHOH ONE END OF THE ENZYME-SEVERED DNA STRAND.
                         Query Match
Best Local
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
COtton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                      Repeat; C
ZN_FING
ZN_FING
ZN_FING
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01131; Topoisom_bac; 1.
Pfam; PF01751; Toprim; 1.
Pfam; PF01396; zf-C4_Topoisom;
PF1NTS; PR00417; PRTPISMRASEI.
SMART; SM00437; TOPIAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA topoisomerase I (EC 5.99.1.2) (Omega-protein) (Relaxing enzyme) (Untwisting enzyme) (Swivelase).
TOPA OR MJ1652
                                                                                                                                                                                                                                                                                                                              SMART; SM00436;
SMART; SM00493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - between Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96337999; PubMed=8688087;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000380;
InterPro; IPR002936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003601;
InterPro; IPR003602;
                                                                                                                                                                                                                                                                           isomerase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   мJ1652;
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                                                                                                                                                                                                                                                 Comp
                            Similarity
                                                                                                                                                                                                                                                                     PS00396; TOPOISOMERASE_I_PROK; 1.
e; Topoisomerase; DNA-binding; Zin
  Conservative
                                                                                                                                                                                                                                               lete
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                                                                                                                                                                                                                                                                                                                                 TOPRIM; 1
                                                                                                                                                                                                                                                                                                                                                           TOP1Bc;
                                                                                                                                                               proteome.
626
706
747
                            11.0%;
27.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pro_topoisomerase
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                                                                                                            MW;
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  115;
Score 573; DB
Pred. No. 1.5e
L5; Mismatches
                                                                                        DNA CLEAVAGE (6) 01
; 2F9C95753E202D82
                                                                                                                          C4-TYPE 1.
C4-TYPE 2.
C4-TYPE 3.
DNA CLEAVAGE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                     Zinc-finger;
  .5e-29;
les 337;
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                                                      DB 1;
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                                             Length
                                                                                                            CRC64;
Indels
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                                                                                                                                                                                                                                                                        Metal-binding;
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Gaps
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19;
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TOP1
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STRAIN-DELTA H;
STRAIN-PEBLTA H;
STRAIN-P8037514; PubMed-9371463;
Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dulandridge T., Bashiradeh R., Blakely D., Cook R., Gilbert K., Aldredge T., Bashiradeh R., Blakely D., Cook R., Gilbert K., Aldredge T., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhake Mandridge R., Shimer G., Goyal A., Pietrovski S., Church G.M.
                                                                                                                                                                                                                                                     DNA topoisomerase I (EC 5.99.1.2 (Untwisting enzyme) (Swivelase). TOPA OR MTH1624.
                                                                                                                                                                                                                                                                                                                                                                               _METTH
                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                      Archaea; Euryarchaeota; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                027661;
16-0CT-2001
                                                                                                                                                                                                                                    Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                             TOP1_METTH
                                                                                                                                                                                      NCBI_TaxID=145262;
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16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                           670
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InterPro; IPR00380; Pro_topoisomerase.
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InterPro; IPR00380; Pro_topoisomerase.
InterPro; IPR00393; Topim; 1.
Pfam; PF01751; Topoisom_bac; 1.
Pfam; PF01396; zf-c4_Topoisom; 2.
PRINTS; PR01396; zf-c4_Topoisom; 2.
PRINTS; PR00417; PRTPISMRASEI.
SMART; SM00436; TOPIAC; 1.
SMART; SM00436; TOPIAC; 1.
SMART; SM00436; TOPIAC; 1.
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ZN_FING
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"Complete genome sequence of Methanobacterium thermoautotrophicum
"ethal: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
-i- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO TOPOISOMERASES LEADS TO TOPOISOMERASES LEADS.
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MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME-SEVERED DNA STRAND.

SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
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QGSDAEVKDVRVRDTIRKPPVPFDLGTLQSEAYRVFGFSPKKTQTIAQNLYTEGYTSYPR
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IPR003601; DNAtopI_ATP_bind.
IPR003602; DNAtopI_DNA_bind.
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C4-TYPE 2.
DNA CLEAVAGE (BY SIMILARITY).
88507CAED59C0307 CRC64;
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                                                                                                                                                              323 TSSOKLPESIGYEKILKNLAKNPRFGVHIERL--RGPLKPHEGKKEDDAHPAIHPTGLLP 380
                                                                                                                                                                         338 TETNIFPRDLNLTVLVEQQTPDPRWGAFAQSILERGGPTPRNGNKSDQAHPPIHPT-KYT 396
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ALIGNMENTS

REFERENCE AUTHORS TITLE TOURNAL MEDLINE REFERENCE AUTHORS TITLE KEYWORDS SOURCE ORGANISM RESULT 1 HSU43431 LOCUS DEFINITION ACCESSION FEATURES VERSION JOURNAL source 2 (bases 1 to 3755)
Hanai, R. and Wang, J.C.
Direct Submission
Submitted (15-DEC-1995) Ryo Hanai, Molecular and Cellular Biology,
Hrvard University, 7 Divinity Avenue, Cambridge, MA 02138, USA
Location/Qualifiers Human DNA topoisomerase U43431 U43431.1 GI:1292911 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3755)
Hanai, R., Caron, P.R. and Wang, J.C.
Human TOP3: a single-copy gene encoding DNA topoisomerase III Proc. Natl. Acad. Sci. U.S.A. 93 (8), 3653-3657 (1996) 96195027 Homo sapiens HSU43431 3755 bp : III mRNA, complete cds. mRNA linear PRI 12-JUL-1996

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RESULT 2
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ORGANISM

AB006074

N Mus musculus mTOP3 mRNA for tc
AB006074
AB006074.1 GI:3061307
mTOP3; topoisomerase III.
Mus musculus (strain:BaLB/c) to Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 3741) Chordata; Rodentia; topoisomerase đđ testis Craniata; Vertebrata; Sciurognathi; Muridae, mRNA CDNA ៥ linear mRNA comp idae; ROD Euteleostomi;
Murinae; Mus 18-APR-1998 cds.

REFERENCE AUTHORS TITLE JOURNAL Seki,T

Direct Submission
Submitted (26-JUL-1997) Takahiko Seki, Tohoku University, of Pharmaceutical Sciences; Aoba Aramaki, Aoba-ku, Sendai 980-77, Japan (E-mail:taka@mail2.pharm.tohoku.ac.jp, Tel:+81-22-217-6876, Fax:+81-22-217-6873) Faculty

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JOURNAL MEDLINE COMMENT FEATURES
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Ramser, J., Mueller, I., Sudbrak; Hennig, S., Francis, F., Steffens Poustka, A., Lehrach, H. and Reiningshiphic
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HTG.
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/clone=1barRPCII.3-5 Human PAC library,
/clone_library RPCII.3-5 Human PAC library,
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de Jong, P. Ioannou"
                 /note="T7_end:PAC RPCI-1 178F10"
34946 c 34918 g 31067 t
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Seranski,P.,
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                                                                                                                                            complete cds.
AF255733
AF255733.1 GI
                                  1 (bases 1 to 3891)
Plank, J.L., Reineke, J.C.
Drosophila melanogaster
                                                                  Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Eukaryota; Meoptera; Endopterygota; Diptera; Brachyce
Muscomorpha; Ephygroidea; Drosophilidae; Drosophila.
   Plank
                        Unpublished
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Drosophila melanogaster
                                                                                                                      fruit fly.
 (bases 1 ank, J.L.,
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Reineke, J.C.,
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Pred. No. 6.6e-172;
                                  topoisomerase
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  Wilson, T.M.
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   AAACATCGGGTTTGAGATTATCCACGTGTGTAAAGGCTGTAAAGCCCAATCTGCAGGTGTT
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                                                                                                                     GCAGCTGGCATTCCAGGTGTCTTACAAAAATTGGAGAACGGTGGATCCGCGCTCTTTATT
                          ACGCGAGGTGCGCGGCTGTCAGGGATTGATTATCTGGACGGATTGCGATCGCGAGGGCGA
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Mismatches

Indels Length

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Gaps

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455 473 395 413 335 353 275 293 215 6; DB 3; 1.1e-147; hes 699;

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Direct Submission
Submitted (13-APR-2000) Biochemistry, Duke University Medical
Center, Research Drive, Durham, NC 27710, USA
                                                           KLSAKETMI JAEKLYTKGF ISYDRTETNOFSKEFALAPLVEMQTGHRDWGAFAQRVIE
WGPNPRNGNKSDOAHPD IHPTKLAENLOGNEARVYELVVHRFLACVSKDAVGSETLVH
ID JAGEKFTANGLVIHERNYLDVYVYDKWSAKQIHYENGQRFEPTEVSLHEGATTAP
PLLTEADLI JALMEKHGIOTDATHAEHINTI KERGY IGVLDKGFLYPGVIGMGLYEGYD
AMELALAKPOLRAEFELDLKLICQGQKDPKVULTEQIAKYKQAYQQITDKI TAMDAKI
SARINETPAANSAVQEGADGSAPSHGI IQSI FQCFKCNEAPLALKPKNOQGWYIGCN
NFPDCKNAAVALFTEKKDASVLDECCPTCGDGYRMLKFRLSTPYYRGVEGTPSGWYKTC
LPCDNLFRTTFNINLDSVKKVGGI VGEVRGGGGGFGPGPGGGGGRGAGSGGWSKFG
GGGGGGGGGGGGGGGGGKKKFRSSKSSFF
GGSGGGGGGGGGGGGGGGGGGGGGGKKKPPTESHALAA
AESVESSSQPKT ISMVPLDDD IAAAFAADDDAEFEALVNGGTMPTESNGDCFDAMLAA
AESVESSSQPKT ISMVPLDDD IAAAFAADDDAEFEALVNGGTMPTESNGDCDLSSLS
EWI KECDKADERPMLAGTTREASJTATTP PPKRAARKREPSSSKYSTGS
APQSTTSWGSNRVVTLFSIQOSNSQRGOSSMRSNSSSTVT ITQTKTKQDERNTATPGD
GEEVMCNCGOLASQLTVRKDGPNGGRPFYACTPREKSCGFFKWGDEPPSSAKSKTGS
APQSTTSWGSNRVVTLFSIQOSNSQRGOSSMRSNSSSTVT ITQTKTKQDERNTATPGD
GEEVMCNCGOLASQLTVRKDGPNGGRPFYACTPREKSCGFFKWGDENDFPNGASSTSWG
GEEVMCNCGOLASQLTVRKDGPNGGRPFYACTPREKSCGFFKWGDENDFPNGASSTSWG
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/note="Top3a"
37. .3789
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RSLFDAPVEKGYGSDYBPIKRTLEREVRGCQGLIIWTDCDREGERIGYEIIDVCRAIK
PNISVYRATFSEITTVAVRRALQQLGQPDKRQSDAVDVFTELDLRTGAAITRFQTMRL
QRLFPEKIADKLISYGSQIPTLGFVAERYKEIEAFVSEPFWKIKVLHTIDDLTVEFN
WARNKLFDKEACENYLLLCLAEPDPRALVESYTYKPKHKWRPTPLDTVEMEKLGSRKL
                                       SANRNPPGRSQPTAITSDGPKTRRCGLCRKEGHTRNKCPRKDEFDM"
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/protein_id="AAF71288.1"
/db_xref="GI:7960302"
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/chromosome="2"
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCTCACCCTCCCATTCACCCCACCAAATACACCAACAACTTACAGGGAGATGAACAGCG
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Allen,C., Adlo-Oduola,B., All-Osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Chen,G., Chen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAPACTAATTTGCCAGGGCCAGAAAGATCCCAAGGTGGTCCTGACCGAACAGATAGCCAA
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AC097545.3
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Muzny,D.M., Adams,C.,
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Mammalia; Eutheria;
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Rodentia;
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(bases

1 to 88718)

Direct Submission Worley, K.C Unpublished

COMMENT

Center code:

BCM

---- Genome Center

findPhrapList

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Submitted (19-CCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:17064400.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 47 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consensus quality: 74659 bases at least Q40
Consensus quality: 79368 bases at least Q30
Consensus quality: 83760 bases at least Q20
Estimated insert size: 66722; sum-of-contigs estimation
Quality coverage: 0.8x in Q20 bases; agarose-fp estimation
Quality coverage: 0.8x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                     Submitted (17-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: Clonerequest@sanger.ac.uk on Nov 20, 2001 this sequence version replaced gi:15865044. During sequence assembly data is compared from overlapping clones
                                                                                                                                                                                                                      Direct Submission
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Best Local Similarity
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                                                                                                TGCCCACCAGGCCCAGGGATCCACCTAGGTGGGTTTGGCAACCCTGGTGATGGCAGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-278121 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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/clone_lib="RPCI-23"
190018. .190031
/note="Sequence from overlapping
(AL596386). Assembly confirmed b
47887 c 49016 g 53216 t
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/db_xref="taxon:10090"
/chromosome="11"
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Pred. No. 1.1e-104;
D; Mismatches 147;
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Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T.,
Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J.,
Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z.,
Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S.,
Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R.,
Gorrell, J.H., Gunaratne, P., Haller, G., Hernandez, J., Hogues, M.,
Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S.,
Kovar, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Martin, R.,
Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morris, S.,
Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Oguh, M., Parish, B.,
Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Watlington, S.,
Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,
Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,
Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,
Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,
Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,
Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,
Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,
Williamson, A., Wrensford, G., Scherren, F., Weinstock, G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-JUN-2000) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On Jun 25, 2001 this sequence version replaced gi:13162471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wases 1 to 213913)
Worley,K.C.
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Worley,K. and Gibbs,R.
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This is a 'working draft' sequence. It currently
consists of 5 contigs. The true order of the pieces
                                                                        NOTE: Estimated insert size may differ from sequence length
                                                                                                                     Chemistry: Dye-primer Bodipy: 49% of reads chemistry: Dye-terminator Big Dye: 51% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 215914 bases at least Q40 Consensus quality: 218176 bases at least Q30 Consensus quality: 219553 bases at least Q20 Estimated insert size: 215987; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 8.2x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: M13; L08821
                                                                                                                                                                                                                                                                                                                                                                                                   Center project Information
Center project name: MAFN
Center clone name: RP23-5201
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Baylor College of
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     TTCCAGTGGGTCGATGAGAACACCGCTCCAGG
                                                                           GGAGGTACACCCTGCCTGTGCGGGCAGCCTGCTGTCACACGGACTGTTCAGAAGGATGGA
                                                                                                                                                                                                                                                       TGCCCATCCAGTGTAGGCAGCCACATGGATGGGTTTGGCCAGCCTTGGCAGCGACAGTGAT
                                                                                                                                                                                                                                                                                                   TGCCCACCAGGCCCAGGGATCCACCTAGGTGGGTTTGGCAACCCTGGTGATGGCAGTGGT
                                                                                                                                                                                                                                                                                                                                                       CATTCCACTGGAGGAGGGACCCCCACCTCTGCATCAGGACCCCCAGGCAGCTCTGTAGGA
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                                                                                                                                                                                                   AGTGGCACATCCTGCCTTTGCAGCCAGCCCTCCGTCACACGGACTGTGCAGAAGGATGGA
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539; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58068
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1. .213913
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/chromosome="11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RP23-5201"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
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80677: gap of unknown length
157388: contig of 76711 bp in 16
157488: gap of unknown length
192191: contig of 34703 bp in 16
192291: gap of unknown length
206716: contig of 14425 bp in 16
206816: gap of unknown length
213913: contig of 7097 bp in length
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77.98;
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Pred. No. 1.1e-104;
0; Mismatches 147;
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6; Gaps

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                                                                                                                                                                    112 CGGAGAGAAGGACTTTCAAAATTCAACAAGATCTATGAATTTGATTATCATCTGTATGGC 171
    232 ATGCAGTTTCGAAAATGGCAGAGCTGCAACCCTCTTGTCCTCTTTGAAGCAGAAATTGAA 291
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12 1 (bases 1 to 87885)

12 1 (bases 1 to 87885)

13 Celniker, S.E., George, R.A., Galle, R.F., Hoskins, R.A., Svirskas, R.R., Harris, N.L., Agbayani, A., Arcaina, T.T., Baxter, E., Svirskas, R.R., Harris, N.L., Agbayani, A., Arcaina, T.T., Baxter, E., Stirskas, R.R., Harris, N.L., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, S.H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Zhang, R., Zieran, L.L., and Rubin, G.M. Sequencing of Drosophila chromosome 2R, region 37E1-37E2 Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGAATGCCAAAATGGTTATGACCTCCGTATCCGGCCACATGATGCAGCTGGCATTCCAG 30779
                                                                                  CAGAATGTTACCATGGTAATGACTTCAGTTTCTGGACATTTACTGGCTCATGATTTCCAG 231
                                                                                                                                                                                                               995;
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Celniker, S.E., George, R.A., Galle, R., Svirskas, R.R., Hoskins, R.A., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Chavez, C., Agbayani, A., Arcaina, T.T., Baxter, E., Flanagan, J., Houston, K.A., Chew, M., Doyle, C.M., Fartan, D.E., Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, S.H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Mok, M.S., Moshrefi, A.R., Maxda, P., Mok, M.S., Moshrefi, A.R., Park, S., Ffeiffer, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Whitelaw, K.R., Yee, A., Zhang, R., Zleran, L.L. and Kimmel, B.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Berkeley, CA 94720 For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://fruitfly.berkeley.edu/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (14-AUG-1998) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On Oct 19, 1998 this sequence version replaced gi:3746040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC005428 87835 bp DNA linear INV 19-OCT-1998 Drosophila melanogaster DNA sequence (Pl DS05231 (D342)), complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Library location: 47-55
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Lawrence Berkeley National Laboratory,
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1 20241 c
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/db_xref="taxon:7227"
/chromosome="2R"
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55.7%;
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20288 g 23808
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                                                                                                                                                                                                           Score 433.4; DB 3;
Pred. No. 2.4e-104;
0; Mismatches 671;
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                                                                                                                                                                                   Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattel, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanenavong, S., Pittman, G. S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.G., Seguencing of Drosophila chromosome 2L, region 37D-37E
2 (bases 1 to 157766)
Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C. Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endoptera; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 157766)
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112 CGGAGAGAAGGACTTTCAAAATTCAACAAGATCTATGAATTTGATTTATCATCTGTATGGC 171
                                                                                                                                                           GAGATCACACCCCATGCCGTCAGGACAGCTTGTGAAAAACCTGACCGAGCCTGATCAGAGG 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGTCTTACAAAAATTGGAGAACGGTGGATCCGCGCTCTTTATTCGACGCGCCGGTGAAA 85595
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                                                          GTGAGCGATGCTGTGGATGTGAGGCAGGAGCTGGACCTGAGGATTGGAGCTGCCTTTACT
                                                                                                                                                                                                                                                                                  ATTATCCACGTGTGTAAAGGCTGTAAAGCCCAATCTGCAGGTGTTGCGAGGCCCGATTCTCT 471
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                                                                                                                                                                                                                                               ATTATTGATGTGTGTCGCGCTATCAAACCGAATATTTCGGTTTATCGTGCCACTTTCTCG
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                                                                                                                                                                                                                                                                                                                                                                                                          TGCCAGGCTCTGGTGATCTGGACTGACTGTGATAGAGAAGGCGAAAACATCGGGTTTGAG 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGTACTGCCCAGAGAATTTTGTAGACATCAAGAAAACTTTGGAACGAGAGACTCGCCAG
                                                                                                                       GAGATTACCACGGTGGCGTGCGTCGGGCTCTGCAGCAATTGGGGCCAGCCGGACAAAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D., Ferriera,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A., Gonzalez,M., Houck,J. Hoskins,R.A., Hostin,D., Howland,T.J., Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A., McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J., Pacagas,V., Park,S., Patel,S., Pfeiffer,B., Phouanenavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F., Stapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M., Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C. Direct Submission
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Sequence submitted by:
Berkeley Drosophila Genome
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
/chromosome="2L"
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/clone_lib="RPCI-98 (Roswell Park Cancer Institute
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ACATCGAGACCATCAAAGCCCGGATGTACGTGGGCCTCACCCCAGACAAGCGGTTCCTCC 1615
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                                                                CCGACCTCATTGCCCTCATGGAGAAGCATGGCATTGGTACGGATGCCACTCATGCGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCAGGAACGCTTTGTGGCCCATGGCCTCATGATTCTGGCCCGAAACTATCTGGATGTGT 1375
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    - AGTAACTCATGACCACAAAGATGGTATCGTAGA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAAATTTGTGGTTCTAAGGCAGCAAGTGCAGAAATACAAGCAGG
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                                                                                                                                                 Venter, E., Wang, A.H., Wang, X., Wang, Z.Y., Wassarman, D.A., Weinstock, G.M., Weissenbach, J., Williams, S.M., Woodage, T., Worley, K.C., Wu, D., Yang, S., Yao, Q.A., Ye, J., Yeh, R.F., Zaveri, J.S., Zhan, M., Zhang, G., Zhao, Q., Zheng, L., Zheng, X. Zhu, S., Zhu, X., Zhu, S., Zhu, X., Smith, H.O., Gibbs, R.A., Myers, E.W., Rubin, G.M. and Venter, J.C. The genome sequence of Drosophila melanogaster Science 287 (5461), 2185-2195 (2000)
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Li,J., Li,Z., Liang,Y., Lin,X., Liu,X., Mattei,B., McIntosh,T.C.,
McLeod,M.P., McPherson,D., Merkulov,G., Milshina,N.V., Mobarry,C.,
Morris,J., Moshrefi,A., Mount,S.M., Moy,M., Murphy,B., Murphy,L.,
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Nusskern,D.R., Pacleb,J.M., Palazzolo,M., Pittman,G.S., Pan,S.,
Pollard,J., Puri,Y., Reese,M.G., Reinert,K., Remington,K.,
Saunders,R.D., Scheeler,F., Shen,H., Shue,B.C., Siden-Kiamos,I.,
Simpson,M., Skupski,M.P., Smith,T., Spier,E., Spradling,A.C.,
Stapleton,M., Strong,R., Sun,S., Switskas,R., Tector,C., Turner,R.,
Venter,E., Wang,A. H., Wang,X., Wang,T.Y., Wassarman,D.A.
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AE003663.2 GI:10
2 (bases 1 Adams, M.D.,
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1 (bases 1 to 299449)
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Celniker, S.E.,
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Hoskins,R.A., Galle,R.F.,
shburner,M., Henderson,S.N.,
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Submitted
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On Oct 9, 2000 this sequence version replaced gi:7298582.
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                  EGVEALAESFKHNPHLRVLNMNDNTLKSEGAEKTAEALPFLPLLREMSFGDCLIKTNG
AYHFGEALERGNERLEVIDLGFNEINSDGGLVLVNAMGNKPKLRILNLDGNSFGEEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FFCGHAAECWEPGSSWALDQAKRNLVNEYFLVGVTEQMYEFVDLLERSLPRIFHGFRE
HYHNSNKSHLRVTSSKLPPSESTIKSIQKTKIWQMENDLYDFALAQFEFNKKKLMQPD
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complement[join(1882. . 2125,2209. .2429,2490. .2628,
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2687. .3005,3071. .3339))
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EKIISEMSKLPTAAALQPFQHQEEEDLEDEYQADKQDADYEEEEEVHEHANDTTEEAL
                                                                                                                                                                                                                                                                                                   transcript"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from the published sequence for this transcript."
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                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                        /note="Sd
                                                                                                                                                                                                                                                                                                                                                                                /gene=":
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Hs2st gene product; Nucleotide sequence of the
celera sequence_differs from the published sequence for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Nucleotide sequence of the Celera sequence differs from the published sequence for this transcript."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="Nucleotide sequence of the Celera sequence differs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcript"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .>5895
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differs from the published sequence for this
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GIPKLEDÄNEAGGKNSIKCTLILTEGDSAKSLÄVSGLGVIGRDLYGVFPLRGKLLNVR
EANFKOLSENARINNLCKIIGLOYKKKYLTEDDLKTLRYGKVLMITDODDOGSHIKGL
LINFIHTNMPELLRLPFLEEFITPIVKATKKNEELSFYSLPEFEEMKNDTANHTYNI
KYYKGLGTSTSKEAKEYFODMORHTLIFKYDGSVDEBSIVMAFSKKHIESRKYMLTNH
MDEVKRRKELGLPERYLYTKGTKSITYADFINLELVLFSNADNERSIPSLVDGLKPGQ
RKVMFTCFKRNDKREVKYADLSGSVAEMSAYHHGEVSLOMTIVLAQNFVGANNINLL
EPRGQFGTRLSGGKDCASARYIFTIMSPLTRLIYHPLDDFLDDYODDGQKIEPLMYL
PIIPMYLVNGAEGIGTGWSTKISNYNBREIMKNLRKMINGQEPSVMHFWXNFLGRME
YVSDGRYIQTGNIQILSGNRLEISELPVGVWTQNYKENVLEPLSNGTEKVKGTISEYR
EYHTDTTVRFYISFAPGEFERHAEEGGFYRVFKFTTTLSTNGNHAEDQNNCLRRFFYI
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MCDELLKRGYRPDPVKEWQRRIKMEDAEQADEEDEEEEAAPSVSSKAKKEKEVDPEK
AFKKLTDVKKFDYLLGMSMWMLTEEKKNELLKQRDTKLSELESLRKKTPEMLWLDDLD
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GEPVEFKITEEIIKKMAAAAKVAQAAKEPKKPKEPKEPKVKKEPKGKQIKAEPDASGD
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LMSRRAYDVAASSKGVSVFLNGNKLGIVHEVANERWEVACCPSDRGFQQVSFVNSIAT
YKGGRHVDHVVDNLIKQLLEVLKKKNKGGINIKPFQVRNHLWVFVNCLIENPTFDSQT
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GQGIPVTMHKEQKMYVPTMIFGHLLTSSNYNDDEKKVTGGRNGYGAKLCNIFSTSFTV
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10075. .10248,10306. .10863))
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/gene="Top2"
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10075..10248,10306..10863,11829..>12084))
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QKCTPEKFCLSQKPCSQEDFDSLDMDNKLEALQSIVNQFTGDNHLLLLVFTTLKCAHL
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16054. .161
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join(15011._15146,15208. .15302,15402. .15746,15806. .15984,
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4.	Uπ ⊨	CAGCTATCCCCGTACGGAAACCAACCAGTTCTCCAAGGAGTTCGCTCTGGCACCACTAGT	9 1	B 2
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74	89 57	GTGTGTGGAGGATCCCATGGCAACTGTGGTAGAGGTCAGATCTAAGCCCAAG		Db Qy
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64	1 779 1 5775	TTGGAAAGCTATAAA	747 57695	ρ Q
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4	\$ 411 \$ 5733	TGCCAGGCTCTGGTGATCTGGACTGACTGTGATAGAGAAGCGAAAACATCGGGTTTGAG	352 57275	P 04
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4	291 5721	ATGCAGTTTCGAAAATGGCAGAGCTGCAACCCTCTTGTCCTCTTGAAGCAGAAATTGAA	232 57155	Db Qy
44	3 231 3 5715	CAGAATGTTACCATGGTAATGACTTCAGTTTCTGGACATTTACTGGCTCATGATTTCCAG	172 57095	ФФ
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                                                                  AGCCTGACCTCCGGGCTGAACTGGAAGCTGATCTGAAGCTGATCTGTGATGGCAAAAAGG
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                         ACAAATTTGTGGTTCTAAGGCAGCAAGTGCAGAAATACAAGCAGG
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REFERENCE AUTHORS TITLE JOURNAL ACCESSION VERSION COMMENT SOURCE KEYWORDS Drosophila melanogaster Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musecomorpha: Ephydroidea; Drosophilidae; Drosophila. Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
This sequence was identified as CDM:10214069 by the submitter. For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence. pieces. AC018257 AC018257.1 GI:6552934 HTG; HTGS_PHASE2. Direct Submission Submitted (09-DEC Adams, M. and Venter, J.C. Muscomorpha; Ephydroidea; fruit fly.

RESULT 11 AC018257 LOCUS

DEFINITION

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                                                             CTGCCTGGCCGAACCCGATCCTAGAGCGCTCGTGGAGAGCGTCACCGTTAAGCCCAAACA
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ACCESSION VERSION KEYWORDS RESULT 12 AF057032 LOCUS SOURCE ORGANISM DEFINITION Caenorhabditis elegans. Caenorhabditis Eukaryota; AF057032.1 AF057032 AF057032 Metazoa; GI:3047012 elegans Nematoda; Chromadorea; 2422 bp mRNA DNA topoisomerase linear III (TOP3) Rhabditida; mRNA, INV 27-APR-2000

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Functional characterization of Caenorhabditis
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/db_xref="GI:3047013"
/tanslation="MKRALFVAEKNDVAKGVAAILSNGTANRREGRSKENKIYTLNTE
/translation="MKRALFVAEKNDVAKGVAAILSNGTANRREGRSKENKIYTLNTE
LFGQQTAISVTSVSGHMMNFQFHENMSNWQTASMVELFRAPVRHVVTPEMKLIEQTLR
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Submitted (05-AUG-1997) Dept. Chemistry, Rikkyo
Nishi-Ikebukuro, Toshima, Tokyo 171, Japan
Kawasaki, K. Genome Res. 7, 250-261, 1997.
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One-megabase sequence analysis of the human immuno
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       TGATGACCCTGGATTTCCTGGGAAAATACAACAAATGGGACAAAGTGGACCCCGCAGAAC
                                                                                                                         TTGATTATCATCTGTATGGCCAGAATGTTACCATGGTAATGACTTCAGTTTCTGGACATT
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                            TACTGGCTCATGATTTCCAGATGCAGTTTCGAAAAATGGCAGAGCTGCAACCCTCTTGTCC
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Ng,S.W., Liu,Y., Hasselblatt,K.T., Mok,S.C. and Berkowitz,R.S. A new human topoisomerase III that interacts with SGS1 protein Nucleic Acids Res. 27 (4), 993-1000 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (09-MAR-1998) OB/GYN Women's Hospital, 221 Longwood
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/db_xref="G1:4321652"
/translation="MKTVLMYAEKPSLAQSIAKILSRGSLSSHKGLNGACSVHEYTGT
FAGQPVRFKMTSVCGHVMTLDPLGKYNKMDKVDPABLFSQAPTEKKEANPKLMNVKFL
FAGQPVRFKMTSVCGHVMTLDPLGKYNKMDKVDPABLFSQAPTEKKEANPKSITDTDI
CNAMACIGEPDHNEALSVDARGELDLRIGGAFTRFQTKYFGGKYGDLDSSLISFGPCQ
TPTLGFCVERHDKIGSEKPETYWVLQAKVNTDKDRSLLLDMDRVRVEDREIAQMFLNM
TKLEKEAQVEATSRKEKAKQRPLALNTVEMLRVASSSLGMGPQHAMQTAERLYTQGYI
SYPRTETTHYPENDLKGSLRQQANHPYWADTVKRLLAEGINRPKGHAAGDHPPITP
MKSATEAELGGDAWRLLYEYITRHFIATVSHDCKYLQSTISFRIGPELFTCSGKTVLSP
GFTEVENWGSVPLEESLPTCQRGDAFFVGEVKNLEKQTNEPDYLTEAELITLMEKHGI
GTDASIPVHINITCORNYTYWESGRRLKPTNLGTULYHGYYKIDAELYLPTIRSAVEK
QLNLIAOGKADYRQVLGHTLDVFKRKEHYFVDSIAGMDELMEVSFSPLAATGKPLSRC
GKCHREMKYIOAKPSRHCSHTDLVFKRKEHYFVDSIAGMDELMEVSFSPLAATGKPLSRC
GKCHREMKYIOAKPSRHCSHTDLFTHFSCQHSLSMLGTGCVECESGVLVLDPTS
GPWKVYACNCNUVAHCFENAHRVRVSADTCSVCEAALLDVDFNKAKSPLPGDETQHM
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/db_xref="taxon:9606"
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                                                        GCGTGCCCCTGGAGGAGAGCCTGCCCACTTGCCAGCGGGGTGATGCCTTCCCTGTGGGCG
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                                                                                                                                                                      TTGTGGCCCATGGCCTCATGATTCTGGCCCCGAAACTATCTGGATGTGTATCCATATGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Gaithersburg, Maryland;
                                                                                                                                                                through the I.M.A.G.
Series: IRAL Plate:
This clone was selec
                                                                                                                                                                                                                                                                              Contact: nisc_mgc@nhgri.nih.góv
ShevChenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (05-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11AO3, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Mammalia; E
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IMAGE: 3346377,
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; Eutheria; F
s 1 to 3133)
/db_xref="taxon:9606"
/clone="MGC:1867 IMAGE:3346377"
                                           /organism="Homo sapiens'
/db_xref="LocusID:8940"
                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:12803238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.nisc.nih.gov/
                                                                                                                                     MGC clone distribution informate. E. Consortium/LLNL at: http://i 5 Row: e Column: 12 cted for full length sequencing selection criteria: matched mF
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                                                                                                                                             mRNA
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MGC:1867
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/tissue_type="Skin,

melanotic

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CCTTTACTAGGTTCCAGACCCTGCGGCTTCAGAGGATTTTTCCTGAGGTGCTGGCAGAGC
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                                                                                                        ATCAGAGGGTGAGCGATGCTGTGGATGTGAGGAGCTGGACCTGGAGGATTGGAGCTG
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TPTLGFCVERHDKIQSEKPETYWVLQAKVNTDKDRSLLLDWDRVRVFDREIAQMFLNM
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GCVFCDPVFQELVELKHAASCHPMHRGGPGRRGGRGRARRPPGKPNPRRPKDKMSA
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                                 CCATGGGCTATGAAATGTCTAAGCCTGACCTCCGGGCTGAACTGGAAGCTGATCTGAAGC
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